

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 02:14:44 ; Search time 36 Seconds

(without alignments)  
306.980 Million cell updates/sec

Title: US-09-308-829-2

Perfect score: 1232  
Sequence: 1 MKKINIKIYFIITVLISF.....KDNRIIMKNFSHPDIYLEK 235

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	95.9	235	1	SPEC_STPRY
2	394.5	32.0	234	1	SPEG_STPRY
3	219	17.8	258	1	ETXD_STAU
4	211	17.1	251	1	SPEA_STPRY
5	185.5	15.1	257	1	ETXE_STAU
6	183	14.9	266	1	ETCX_STAM
7	178.5	14.5	266	1	ETC2_STAM
8	177.5	14.4	257	1	ETXG_STAM
9	175	14.2	258	1	ETXG_STAM
10	171.5	13.9	266	1	ETXB_STAU
11	167.5	13.6	266	1	ETXC_STAU
12	142	11.5	236	1	SPEH_STPRY
13	96.5	7.8	910	1	NNOG_BUCAP
14	95	7.7	635	1	ETFL_YABAM
15	94	7.6	2077	1	TEGU_HSV6
16	93.5	7.6	547	1	ZN81_HUMAN
17	93	7.5	541	1	FOIM_HAERIN
18	93	7.5	751	1	FOH1_PIG
19	93	7.4	430	1	YVCF_ECOLI
20	91	7.4	3343	1	YOG7_CAEBL
21	90.5	7.3	212	1	DSBA_BUCAI
22	90.5	7.3	948	1	RPOP_PODAN
23	90	7.3	715	1	UYRD_MCPN
24	90	7.3	2077	1	TEGU_HSV6
25	89	7.2	346	1	SYM_CHTNR
26	89	7.2	492	1	ATPB_PSINU
27	89	7.2	569	1	CYSP_PLAFA
28	89	7.2	590	1	MP44_YIDY
29	89	7.2	670	1	PBP_STAU
30	87.5	7.1	831	1	RPOP_GEISP
31	87.5	7.1	2869	1	RBP1_PLAYB
32	87	7.1	366	1	MURA_BUCAP
33	87	7.1	481	1	ATPB_MESVI

34	87	7.1	559	1	ENS2_YEAST
35	87	7.1	602	1	PEF2_LACIC
36	87	7.1	603	1	5MTD_HAERIN
37	86.5	7.0	432	1	Y221_METUA
38	86.5	7.0	463	1	SYC_MIGBR
39	86.5	7.0	1104	1	COLA_CLOPE
40	86	7.0	382	1	PORL_BUCAI
41	86	7.0	490	1	ATPB_CUSRE
42	86	7.0	492	1	ATPB_ANCLX
43	86	7.0	521	1	SYM_DREPA
44	86	7.0	524	1	Y395_MYCCE
45	86	7.0	792	1	Z328_HUMAN

## ALIGNMENTS

RESULT 1	ID	SPEC_STPRY	STANDARD:	PRT:	235 AA.
AC	P13380:				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Exotoxin type C precursor (SPE C).				
GN	SPEC OR SPY0711.				
OS	Streptococcus pyogenes.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OX	Streptococcus.				
NCBI_TaxID=1314:					
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.				
RC	STRAIN-T18P / MGAS 1585.				
RA	Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;				
RA	MEDLINE=88314303; PubMed=3045005;				
RA	Goshorn S.C., Schlievert P.M.;				
RT	"Nucleotide sequence of streptococcal pyrogenic exotoxin type C.;"				
RL	Infect. Immun. 56:2518-2520(1988).				
RN	[2]				
RP	REVISIONS TO 21-26.				
RC	STRAIN-T18P / MGAS 1585.				
RX	MEDLINE=92363541; PubMed=1500157;				
RA	Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;				
RT	"Molecular population genetic evidence of horizontal spread of two				
RT	alleles of the pyrogenic exotoxin C gene (spec) among pathogenic				
RL	clones of Streptococcus pyogenes.;"				
RN	Infect. Immun. 60:3513-3517(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SF370 / ATCC 700294 / Serotype M1;				
RX	MEDLINE=21192684; PubMed=11296296;				
RA	Perrett J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,				
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,				
RA	Yuan Y., Jia H.G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,				
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;				
RT	"Complete genome sequence of an M1 strain of Streptococcus				
RT	pyogenes.;"				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.				
RX	MEDLINE=97397352; PubMed=9253413;				
RA	Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;				
RT	"Crystal structure of the streptococcal superantigen SPE-C:				
RT	dimerization and zinc binding suggest a novel mode of interaction				
RT	with MHC class II molecules.;"				
RL	Nat. Struct. Biol. 4:635-643(1997).				
CC	-I- SUBUNIT: Binds to major histocompatibility complex class II beta				
CC	chain.				
CC	-I- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE				
CC	THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET				
CC	FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE				
CC	DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC				
CC	FEVER.				
CC	-I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.				

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-!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
FAMILY.
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-----
DR EMBL: M35514; AAA27017.1; ALT_SEQ.
DR EMBL: M97156; AAB59091.1; -.
DR EMBL: M97157; AAB59092.1; -.
DR PIR: A30508; A30509.
DR PIR: A44799; A44799.
DR PDB: 1AN8; 29-APR-98.
DR PDB: 1KTK; 07-JUN-02.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_toxin.
DR Pfam: PF02876; Staph_tox_C; 1.
DR Pfam: PF01123; Staph_tox_C; 1.
DR PRINTS: PR00279; BACRRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 235 EXOTOXIN TYPE C.
FT CONFLICT 53 53 N -> D (IN REF. 1).
FT HELIX 33 44
FT STRAND 49 59
FT STRAND 63 67
FT HELIX 69 72
FT TURN 74 75
FT STRAND 77 81
FT HELIX 84 87
FT TURN 88 89
FT TURN 92 93
FT STRAND 95 100
FT TURN 108 109
FT STRAND 110 114
FT STRAND 117 119
FT STRAND 127 128
FT STRAND 131 135
FT TURN 136 137
FT STRAND 141 142
FT TURN 144 145
FT STRAND 148 149
FT STRAND 153 155
FT HELIX 156 171
FT TURN 173 174
FT TURN 176 177
FT STRAND 182 189
FT TURN 190 191
FT STRAND 194 198
FT TURN 204 205
FT HELIX 213 217
FT STRAND 220 222
FT HELIX 223 225
FT STRAND 226 235
SQ SEQUENCE 235 AA; 27371 MW; 070534AAB952C1E0 CRC64;

Query Match 95.9%: Score 1182; DB 1; Length 235;
Best Local Similarity 97.0%: Pred. No. 7.5e-84;
Matches 228; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 MKKINIKIYFIITIVILISTFTYHQSDSKDKDISNVKSDLLYATITPYDKDCRVNFST 60
|||||
1 MKKINIKIYFIITIVILISTFTYHQSDSKDKDISNVKSDLLYATITPYDKDCRVNFST 60

```

QY		61	HTHLLIDIQKYGKDYIISSEMSYFASQFKRDDHDVGLGFYLINSHTGEVIYGGITPA	120
Dd		61	THTLNLDIQKYNGKRYIISSEMSYFASQFKRDDHDVGLGFYLINSHTGEVIYGGITPA	120
QY		121	ONNKYNHKLLGNLFTSGESQOOLNNKIILEKDIIVTFQEIDFKIRKYLMDNYKIYDATSPY	180
Dd		121	ONNKYNHKLLGNLFTSGESQOOLNNKIILEKDIIVTFQEIDFKIRKYLMDNYKIYDATSPY	180
QY		181	VSGRIEIGTKGKHQHOIDLFDOSPNGTSTRSDFAKKYNDNIIMKNKNSHDDIYLEK	235
Dd		181	VSGRIEIGTKGKHQHOIDLFDOSPNGTSTRSDIFAKYDKNRINIMKNNSHPDIIYLEK	235
<hr/>				
	RESULT 2			
	SPEG_STRPY	ID	STANDARD:	PRT: 234 AA.
AC	Q9XSC7			
Dt	16-OCT-2001	(Rel. 40,	Created)	
Dt	16-OCT-2001	(Rel. 40,	Last sequence update)	
Dt	16-OCT-2001	(Rel. 40,	Last annotation update)	
DE	Exotoxin type G precursor (SPE G).			
GN	SPEG OR SPY0212.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OX	Streptococcus.			
OX	NCB1_TaxID=1314;			
RC	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=M1.			
RA	Protein=99093428; PubMed=9874566;			
RA	Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;			
RT	"Identification and characterization of novel superantigens from			
RT	Streptococcus pyogenes.";			
RL	J. Exp. Med. 189:89-102(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;			
RC	MEDLINE=21192684; PubMed=11296296;			
RX	Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RL	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
CC	-I- SUBUNIT: Binds to major histocompatibility complex class II beta			
CC	chain.			
CC	-I- DISEASE: Mitogenic for human peripheral blood lymphocytes.			
CC	-I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isdb.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: AF124499; AAD30988.1; -			
DR	EMBL: AE006489; AAA33303.1; -			
DR	HSSP: P13380; IAN8.			
DR	InterPro: IPR006177; Bctrl_tox.			
DR	InterPro: IPR006123; Staph/Strep_toxin.			
DR	InterPro: IPR006126; Staph/Strep_tox.			
DR	InterPro: IPR006173; Staph_tox_OB.			
DR	Pfam: PF02876; Staph_Stp_tox_C; 1.			
DR	Pfam: PF01123; Staph_Stp_toxin; 1.			
DR	PRINTS: PR00279; BACTRLOTXIN.			
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.			
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Toxic; Signal; Complete proteome.			
TM	SIGNAL 1 24 POTENTIAL.			



RX MEDLINE-21927593; PubMed-11917108;  
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,  
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,  
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
RA Kapur V., Daly J.A., Yeasty L.G., Musser J.M.,  
RT "Genome sequence and comparative microarray analysis of serotype M18  
RT group A Streptococcus strains associated with acute rheumatic fever  
RT outbreaks";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).  
RX MEDLINE-99094887; PubMed-9878045;  
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,  
RA O'Brien S.M., Tranter H.S., Acharya K.R.,  
RT "Structural basis for the recognition of superantigen streptococcal  
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell  
RT receptors";  
RL EMBO J. 18:9-21(1999).  
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta  
CC chain.  
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE  
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET  
CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE  
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC  
CC FEVER.  
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.  
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
CC FAMILY.  
CC -----  
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CC -----  
DR EMBL: U40453; AAC4868.1; -  
DR EMBL: X03929; CA427568.1; -  
DR EMBL: AE009982; AAL97141.1; -  
DR PDB: 1B12; 24-NOV-99.  
DR PDB: 1FNU; 17-NOV-00.  
DR PDB: 1FNU; 17-NOV-00.  
DR PDB: 1FNU; 17-NOV-00.  
DR PDB: 1H45; 03-APR-02.  
DR PDB: 1LOX; 03-APR-02.  
DR InterPro: IPR006177; Bcrl1\_tox.  
DR InterPro: IPR006123; Staph/Strep\_toxin.  
DR InterPro: IPR006126; Staph/Strep\_tox.  
DR InterPro: IPR006173; Staph\_tox\_08.  
DR Pfam: PF02876; Staph\_tox\_C; 1.  
DR Pfam: PF01123; Staph\_tox\_C; 1.  
DR PRINTS: PR00279; BACTRLOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Toxin; Signal; 3D-structure; Complete proteome.  
FT SIGNAL 1 30  
FT CHAIN 31 251  
FT DISULFID 117 128  
FT FT  
FT CONFLICT 6 6  
FT CONFLICT 17 18  
FT CONFLICT 25 35  
FT CONFLICT 40 40  
FT CONFLICT 43 43  
FT CONFLICT 47 59  
FT FT  
FT CONFLICT 129 129  
FT CONFLICT 165 178  
FT FT  
FT HELIX 36 38  
FT HELIX 42 44  
FT TURN 48 48  
FT HELIX 49 56  
FT HELIX

FT STRAND 60 66  
FT STRAND 69 69  
FT TURN 73 74  
FT STRAND 75 78  
FT STRAND 82 82  
FT TURN 83 84  
FT STRAND 85 85  
FT STRAND 87 91  
FT HELIX 95 101  
FT TURN 102 103  
FT STRAND 105 110  
FT STRAND 113 113  
FT TURN 115 116  
FT STRAND 126 130  
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FT TURN 137 138  
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FT TURN 154 155  
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FT STRAND 169 171  
FT HELIX 172 187  
FT STRAND 199 205  
FT STRAND 212 215  
FT HELIX 224 227  
FT TURN 228 231  
FT TURN 232 233  
FT STRAND 236 238  
FT TURN 239 241  
FT STRAND 243 249  
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBEC3 CRC64;  
Query Match 17.1%; Score 211; DB 1; Length 251;  
Best Local Similarity 27.8%; Pred. No. 2-1e-09;  
Matches 72; Conservative 54; Mismatches 91; Indels 42; Gaps 14;  
QY 2 KINIKIKYFITYVLLISTYFT-----YHSDSKKDISNVKSDLLAVYTTTP 48  
DB 5 KKV-LKKWFEVLYVFLGLTISQEVFAQQDDPSQLHRSYVKNLQNT----YFLYEDDP 59  
QY 49 YDKDCR-VNSTHTTNDIDQKYGKDY-YISSMSVSAQKFRKDHDVDFGL-FYIL 105  
DB 60 VTHENVKSVDDLHSDLIYNS--GPNYDKLTQLKQEMATYLFKDKNVQYGVGYHL 116  
QY 106 ----NSHTGEIXYGITPAQNNKYNH-----KLGNLFISGESQONLNKILLEKDIYT 155  
DB 117 CYLCENARSACITGVY---NHGCHLEIKKIYVKKYSIDG--IQSLFDLETNKKAVT 171  
QY 156 FOEIDFKIRKILMDNKKYI-DATSPYVSGRIEIGTKDGKHQDILFDSPNEGTSDIFAK 214  
DB 172 AQEDYKVKRYLTDNKKQLYTNGPSKYETGYIKFIKPKNESFWDFEPPF-EFTQSKYIMI 230  
QY 215 YKDNRIIMKNKNSHDIYL 233  
DB 231 YKDNETLD-SNISOIEVYL 248  
RESULT 5  
FTXZ STAAU  
ID ETXZ STAAU STANDARD: PRT: 257 AA.  
AC P12993:  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Enterotoxin type E precursor (SEE).  
GN ENTE.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.  
RC STRAIN=MJ8265;  
RX MEDLINE-88257005; PubMed-3384800;  
RA Couch J.L., Solits M.T., Betley M.J.;

RT "Cloning and nucleotide sequence of the type E staphylococcal  
RT enterotoxin gene.";  
RL J. Bacteriol. 170:2954-2960(1988).  
RN [2]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE=96022987; PubMed=7552730;  
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;  
RT "Residues defining V beta specificity in staphylococcal  
RT enterotoxins.";  
RL Nat. Struct. Biol. 2:680-686(1995).  
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary  
CC for the toxin interaction with MHC class II (by similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
CC FAMILY.  
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CC -----  
CC EMBL: M21319; AAA26617.1; -  
CC PIR: A28179; A28179.  
CC PDB: LSRE; 15-OCT-95.  
DR InterPro: IPR006177; Bcctl\_tox.  
DR InterPro: IPR006123; Staph/Strep\_toxin.  
DR InterPro: IPR006126; Staph/Strept\_tox.  
DR InterPro: IPR006173; Staph\_tox.OB.  
DR Pfam: PF02876; Staph\_Strep\_tox.C; 1.  
DR Pfam: PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS: PR00279; BACTRLETOXIN.  
DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;  
KW 3D-structure.  
FT SIGNAL 1 27  
FT CHAIN 28 257  
FT METAL 211 257  
FT METAL 249 251  
FT METAL 251 251  
FT METAL 33 35  
FT HELIX 39 41  
FT STRAND 42 42  
FT TURN 46 47  
FT HELIX 48 51  
FT HELIX 52 54  
FT STRAND 59 64  
FT TURN 66 67  
FT STRAND 69 69  
FT TURN 73 74  
FT STRAND 75 79  
FT TURN 83 84  
FT STRAND 90 94  
FT STRAND 98 104  
FT HELIX 105 106  
FT STRAND 109 113  
FT STRAND 115 116  
FT TURN 118 119  
FT STRAND 128 132  
FT STRAND 135 137  
FT TURN 139 140  
FT STRAND 142 142  
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FT STRAND 171 171  
FT STRAND 173 175

FT HELIX 176 190  
FT TURN 191 191  
FT STRAND 203 211  
FT STRAND 219 221  
FT STRAND 227 227  
FT STRAND 234 239  
FT HELIX 242 244  
FT STRAND 245 247  
FT TURN 249 257  
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;  
Query Match 15.1%; Score 185.5; DB 1; Length 257;  
Best Local Similarity 26.3%; Pred. No. 2e-07;  
Matches 74; Conservative 45; Mismatches 87; Indels 75; Gaps 15;  
QY 1 MKKINIKIVFITVLLISTFYFHOSDSKIDS-----NWSDL-LIAY-- 44  
DB 1 MKKTAFILLLFI--ALTLTSPLVNGSEKSEENEDLRKSELQNALSLNRQIYYNE 58  
QY 45 -TTPYDYKDCRY-----NESTH---TLNID-----TQYRGQDYISMSYE 85  
DB 59 KATTEKESDDQPLENTLLEFKGFETGHPMYNDLVLGSKDATNKYKGR----- 107  
QY 86 ASQKFKRDDHVDVFGLEFYILNSHTG-----EYIYGGITPAONNNVNH--KLGLNFIQGE 138  
DB 108 -----KVDLYGAYYGQACGTPNKTACMYGCVTLHDNNRLTEKKVPINLWIDCK 158  
QY 139 SQQNLNKKIILEEDYTFQEDIEKIRKYLMDNKKITDASPVSQRIEIG-----TKDKR 193  
DB 159 QTTVPIDKVKTSKREYTVQELDQARHYLHGKGLYNSDS--FGKRVGGLIVFHSSEGS 216  
QY 194 HEQIDLFDSPNECTRSDFPAK-YKDNRIITNMKNSHFIDYL 233  
DB 217 TVSYDLPDA--QGYPTDLIRIYRDKNTINSENL-HIDLYL 254  
RESULT 6  
ETC3\_STAMM STANDARD: PRT; 266 AA.  
ID ETC3\_STAMM  
AC P23313;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Enterotoxin type C-3 precursor (SEC3).  
GN EMT3 OR S4V2009 OR SA1817  
OS Staphylococcus aureus (Strain M450 / ATCC 700699),  
OS Staphylococcus aureus (Strain M315), and  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; staphylococcus.  
OX NCBI\_TaxID=158878, 158879, 1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M450 / ATCC 700699, and N315;  
RC MEDLINE=21311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,  
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,  
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RT aureus.";  
RL Lancet 357:1225-1240(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=90220508; PubMed=2325627;  
RA Hovde C.J., Hackett S.P., Bohach G.A.;  
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:  
RT sequence comparison of all three type C staphylococcal  
RT enterotoxins.";  
RL Mol. Gen. Genet. 220:329-333(1990).  
RN [3]

```

RX X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RP MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malchiodi E.L., Li H., Yseun X., Stauffer C.V.,
RA Christlevert P.W., Karjalainen K., Marluza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL Nature 384:188-192(1996).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
-----
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-----
DR EMBL: AP003364; BAB51871.1; -
DR EMBL: AP003135; BAB30997.1; -
DR EMBL: X51661; CA935972.1; -.
DR PIR: S11885; S11885.
DR PDB: 1JCK; 12-NOV-97.
DR PDB: 1KLG; 02-AUG-02.
DR PDB: 1KLU; 14-AUG-02.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_Ltox.
DR InterPro: IPR006173; Staph_Ltox_0B.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
KW Complete proteome.
FT SIGNAL 1 27
FT CHAIN 1 266
FT DISULFID 120 137
FT FT 266
SQ SEQUENCE 266 AA; 30671 MW; 5EDBA32D11FCA59 CRC64;
ENTEROTOXIN TYPE C-3.
Query Match 14.9%; Score 183; DB 1; Length 266;
Best Local Similarity 26.7%; Pred. No. 3.2e-07;
Matches 68; Conservativity 48; Mismatches 105; Indels 34; Gaps 11;
Oy 2 KINIKIRIVFITVL-IST--VFYYHQSDSKRDISNVKSIDLVAVTTPDYKDCRVNF 58
| : : : : | : | | | | : : : : : : : : : : : : : : : : : : : : : :
Db 3 KRLEFSRIYLIFALLIVISTPNVLAESQPDMPDDLLHSSEFTGTMGMKKILTYDHVISA 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 59 S-----THHTL-NIDTKYRKGDYYISSENSYEASQFKRRDHDVDFGLFIINSH 108
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 TKVSVDFKLHADHLINYISDKRLKNYDKVKTELLNEDLAKKYK-DEVVDYGSNNYVNCY 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 109 -----AG--EYIGGTTPAONNKVNKILGNLFISESOQNLNKKITILE----KD 152
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 FSSKDNQGVKTGGCTMGITKEHGNEFDNGNLQNVLV--RYVENKRNLTISFEVDTK 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 153 IVTFQELDFKTRKLYLMNDMYKTYD-ATSPYVSGRIEGTGKDGKHQEIQLDFDSPNEG-TRSD 210
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 180 SVTAQELDIKARNFLINKKNLYEFNSSPYDEGYIKFTINNONTFMFYDMAPAGDKFDISK 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 211 IFAKYKDNRIINMKN 225
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 YLMAYNDNRKTVDSKS 254
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Enterotoxin type C-2 precursor (SEC2).
GN	ENTC2.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX	MEDLINE=89277549; PubMed=2543637;
RA	Bonach G.A., Schlievert P.M.;
RT	"Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2."
RL	Infect. Immun. 57:2249-2252(1989).
RP	[2]
RN	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX	MEDLINE=96027099; PubMed=7582894.
RA	Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RT	Breim R.D., Tranter H.S.;
RL	"Crystal structure of the superantigen enterotoxin C2 from Staphylococcus aureus reveals a zinc-binding site."
RP	Structure 3:769-779(1995).
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX	MEDLINE=96022987; PubMed=7552730.
RA	Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT	"Residues defining V beta specificity in staphylococcal enterotoxins."
RL	Nat. Struct. Biol. 2:680-686(1995).
RN	[4]
RP	COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX	MEDLINE=97334373; PubMed=9191070.
RA	Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT	"A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity."
RL	J. Mol. Biol. 269:270-280(1997).
CC	-1- COPACOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION SYMPTHOCOCAL FOOD POISONING SYNDROME.
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
CC	CC
DR	PIR: A60114; A60114.
DR	PDB: 1STE; 23-DEC-96.
DR	PDB: 1SE2; 08-MAR-96.
DR	PDB: 1COV; 19-SEP-01.
DR	PDB: 1I4P; 19-SEP-01.
DR	PDB: 1I4Q; 19-SEP-01.
DR	PDB: 1I4R; 19-SEP-01.
DR	PDB: 1I4X; 19-SEP-01.
DR	InterPro: IPR006177; Bctrl_tox.
DR	InterPro: IPR006123; Staph/Strep_toxin.
DR	InterPro: IPR006126; Staph/Strep_tox.
DR	InterPro: IPR006173; Staph_tox_OB.
DR	Pfam: PF02876; Staph_Strep_tox_C; 1.
DR	Pfam: PF01123; Staph_Strep_toxin; 1.
DR	PRINTS: PR00279; BACTRLTOXIN.
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc; 3D-structure.
KW	KW
FT	SIGNAL 1 27
FT	CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT	DISULFID 120 137
FT	METAL 36 ZINC.
FT	METAL 110 ZINC.
FT	METAL 145 ZINC.
FT	METAL 149 ZINC.
FT	HELIX 35 37
FT	HELIX 41 43

CC Bacteria, Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=196620, 1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MM2;  
 RX MEDLINE=22040717; PubMed=12044378;  
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hiramatsu K.;  
 RT "Genome and virulence determinants of high virulence community-  
 RT acquired MRSA.";  
 RN Lancet 359:1819-1827(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FR137;  
 RX MEDLINE=88086892; PubMed=3335483;  
 RA Betley M.J., Mekalanos J.J.;  
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene";  
 RN J. Bacteriol. 170:34-41(1988).  
 RN [3]  
 RP SEQUENCE OF 25-257.  
 RX MEDLINE=87222293; PubMed=3584106;  
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;  
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";  
 RN J. Biol. Chem. 262:7006-7013(1987).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95354648; PubMed=7628431;  
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlstien M., Kalland T.,  
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;  
 RT "Crystal structure of the superantigen staphylococcal enterotoxin  
 RT type A.";  
 RN EMBO J. 14:3292-3301(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=97113025; PubMed=8943278;  
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlstien M.,  
 RA Abrahamsen L.;  
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with  
 RT zn2+ at 2.7-A resolution. Implications for major histocompatibility  
 RT complex class II binding.";  
 RN J. Biol. Chem. 271:32212-32216(1996).  
 RN [6]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=96022987; PubMed=7552730;  
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;  
 RT "Residues defining V beta specificity in staphylococcal  
 RT enterotoxins.";  
 RN Nat. Struct. Biol. 2:680-686(1995).  
 RN [7]  
 RP COMPARISON OF STRUCTURE OF SEA AND SBC2.  
 RX MEDLINE=97334373; PubMed=9191070;  
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;  
 RT "A structural and functional comparison of staphylococcal  
 RT enterotoxins A and C2 reveals remarkable similarity and  
 RT dissimilarity.";  
 RN J. Mol. Biol. 269:270-280(1997).  
 RL CC -I- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary  
 CC for the toxin interaction with MHC class II.  
 CC -I- SUBUNIT: Monomer.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.  
 CC -I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
 CC FAMILY.  
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DR EMBL: AP004828; BAB95754.1; -

DR EMBL: M18970; AAA26681.1; -

DR PIR: A28664; A28664.

DR PDB: 1SEF; 11-JUL-96.

DR PDB: 1SXT; 19-NOV-97.

DR PDB: 1DYO; 21-FEB-02.

DR PDB: 1I4G; 21-MAR-01.

DR PDB: 1I4H; 21-MAR-01.

DR PDB: 1I0S; 18-DEC-02.

DR PDB: 1SEA; 15-OCT-95.

DR InterPro: IPR006177; Bcrl\_tox.

DR InterPro: IPR006123; Staph/Strep\_toxin.

DR InterPro: IPR006126; Staph/Strep\_tox.

DR InterPro: IPR006173; Staph\_tox\_OB.

DR Pfam: PF02876; Staph\_tox\_C; 1.

DR Pfam: PF01123; Staph\_tox\_OB; 1.

DR PRINTS: PR00279; BACTRTOXIN.

DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.

DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc; 3D-structure; Complete proteome.

FT STGNL 1 24

FT CHAIN 25 257 ENTEROTOXIN TYPE A.

FT DISULFID 120 130

FT METAL 211 211 ZINC.

FT METAL 249 249 ZINC.

FT METAL 251 251 ZINC.

FT CONFLICT 242 242 T -> S (IN REF. 3).

FT HELIX 28 31

FT TURN 32 33

FT HELIX 39 41

FT TURN 44 45

FT HELIX 46 55

FT TURN 56 56

FT STRAND 59 65

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 78

FT TURN 79 80

FT STRAND 90 94

FT HELIX 98 104

FT TURN 105 106

FT STRAND 108 116

FT TURN 118 119

FT TURN 125 126

FT STRAND 128 132

FT STRAND 135 137

FT TURN 139 140

FT STRAND 142 149

FT STRAND 151 155

FT TURN 156 157

FT STRAND 158 160

FT HELIX 164 166

FT STRAND 167 171

FT STRAND 173 175

FT HELIX 176 191

FT TURN 193 194

FT HELIX 197 199

FT TURN 200 200

FT STRAND 205 212

FT TURN 221 221

FT TURN 223 223

FT HELIX 230 233

FT TURN 234 237

FT STRAND 238 239

FT STRAND 242 244

FT STRAND 248 255

SO SEQUENCE 257 AA; 29669 MW; ADBF5BCA1F14677 CRC64;

Query Match 14.4%; Score 177.5; DB 1; Length 257;

Best Local Similarity 26.8%; Pred. No. 8e-07;

Matches 63; Conservative 39; Mismatches 74; Indels 59; Gaps 13;

QY 24 YHSDSKKDISNVKSDLLVAVTI-----TPYD-YKCRNPFSTHTLNDTKYGRKDY 76

Db 54 YYNEKAKTENKESHQFLQHTLLFKGFDFDSNYNDLVDPSKDIWD---KYRGK-- 107

QY 77 YISEMSYEASQKFRDHDVDFGLFYILNSHTG-----EYIGGITPAQNNKVNH--KL 129

Db 108 -----KVDLYGAYGYCAGGTPKTCAMYGATLHDNNLTLEKKV 149

QY 130 LGNLFIGESQQLNKKIILE-----KDIYFPEIDFKIRKYMDNKYIDATSPYVSGR 184

Db 150 PIVMLMDGK-----QNTVPLETVTKNNKNTVQELDQARKRYQEKRYNYN--SDVFQDK 202

QY 185 IEIG-----TKDKHEQIDLFDSPNEGTRSDIFAK-YKDRITNMKNFSHFIDYL 233

Db 203 VQGLIYFHTSTEPSVNYDLFGA--QGQYSNTILRLIRYRDKTKTINSENM-HIDITL 254

RESULT 9

ETXG\_STAM

ID ETXG\_STAM STANDARD; PRT; 258 AA.

AC 085382;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Enterotoxin type G precursor (SEG).

GN ENTG OR SEG OR SAV1824 OR SA1642.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N315), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI\_TaxID=158878, 158879, 1280;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=FR1572.

RA MEDLINE=98298056; PubMed=9632603;

RT Munson S.H., Tremaine M.T., Beclay M.J., Welch R.A.;

RT Identification and characterization of staphylococcal enterotoxin

RT types G and I from Staphylococcus aureus.;

RL Infect. Immun. 66:3337-3348(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Mu50 / ATCC 700699, and N315;

RA MEDLINE=21311952; PubMed=11418146;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus.;"

RL Lancet 357:1225-1240(2001).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

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CC -----

DR EMBL: AF064773; AAC26660.1; -

DR EMBL: AP003363; BAB57986.1; -

DR EMBL: AP003135; BAB42910.1; -

DR PIR: G89968; G89968.



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DR HSSP: P01552; 1SB2.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF02876; Staph_tox_C; 1.
DR Pfam: PF01123; Staph_tox_08.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258
FT DISULFID 116 133
FT SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;

Query Match 14.28; Score 175; DB 1; Length 258;
Best Local Similarity 23.28; Pred. No. 1.3e-06;
Matches 64; Conservative 57; Mismatches 91; Indels 64; Gaps 12;

QY 1 MKRNIKIYFIIITVILISTYFTYHOSDKDISNVSD-----LLYATTIPYD 50
DB 1 MKRSTVITLILIEYFHNMYNAOPDKLDELNKVDKKNKGTMGNVNLTSPPVE 60
QY 51 YKDCRVNFTHTLIDTOKYRGKDYIISSEMSYEASQKFK-----RBDHYDV 98
DB 61 GRGV-----INSRQFLSHDLFFPIE--YKSYNEVTELENTLANNYDKKVDI 107
QY 99 FGL--FY-----ILNSHGEYIYGGITPAONKNVNHKLGNLFISGESQONLNK 146
DB 108 FGVPYFTCAIIPKSEPDINONFGGCMYGGITFENSSENERDKLI-TVQVTFIDNRQSLGFT 166
QY 147 IILEKDIIVFOEIDFKIRKILMDNYKITYDAF--SPYVSGRIEIGRKDGHEIDFDSFNE 205
DB 167 ITTNKNVITIOELDYKARHMLTEKKLYEFGSAFESGGLKFTKKNNTSEWDFL----- 221
QY 206 GTRSDI--FAKYK-----DNRIIMKNKFSHFIDYL 233
DB 222 -PKKELVPYFYPKFLNLYGDKNKVDSKSIK-MEYFL 255

RESULT 10
ETC1_STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN EMTCL.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: X05815; CAA29260.1; -.
DR PIR: S06356; ENSRCL.
DR HSSP: P34071; 1SB2.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF02876; Staph_tox_C; 1.
DR Pfam: PF01123; Staph_tox_08.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 137
FT CONFLICT 177 177
FT SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;

Query Match 13.98; Score 171.5; DB 1; Length 266;
Best Local Similarity 25.78; Pred. No. 2.4e-06;
Matches 67; Conservative 49; Mismatches 102; Indels 43; Gaps 12;

QY 1 MKRNIKIYFIIITVILISTYFTYHOSDKD-----ISNVKSDLV-AY 44
DB 1 MKRSFISCVLILIALIIVFTPNVLAESQDPPELDLHKSKTKTGLMENKK--VLIDDH 58
QY 45 TTPDYDKDCRVNFTHTL--NIDTOKYRGKDYIISSEMSYEASQKFKRBDHYDVGLF 102
DB 59 YVSAFTKVKSS--VDKFLADLIYINISDKKLKMYD--KVKELLNEGLAKKYKDEVDVYGSN 115
QY 103 YILNSH-----IG--EYIYGITPAONKNVNHKLGNLFISGESQONLNKTIILE 150
DB 116 YVANCYFSSKDNVKGKYGKTCMYGKITRKHGNEHDMGNLONVLI--RVYENKRTISFE 173
QY 151 ----KDIYFQEIIRKIRKILMDNYKITYD--ATSPYVSGRIEIGRKDGHEIDFDSFNE 205
DB 174 VQTRKSKSTYAOELDKARHMLTEKKLYEFGSAFESGGLKFTKKNNTSEWDFL----- 223
QY 206 G-TRSDIFAKYKDNRIIMKN 225
DB 234 KFDQSKYLMYNDNKTVDSKS 254

RESULT 11
ETXB_STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
```



Db	166	DGKNILSPDQVTKNKKVTAQGLDYLTRHYILVKNKKLKEFNNSPETYGIKRIENENSP-W	22	224
Oy	197	IDLFDSPNEG-TRSDIPAKYDNKILNNKNSHSDIYL	233	
Db	225	YDKMPAPGDKFDQSKYLLMNYDNKNKVDKVK-IEVYL	261	
RESULT 12				
SPFH_STRPY	STANDARD:	PRT:	236 AA.	
AC	Q9X5C8:			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Exotoxin type H precursor (SPE H).			
GN	SPFH OR SPY1008.			
OC	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OX	Streptococcus.			
OX	NCHI_TaxID=1314;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=M15;			
RC	MEDLINE=99093428; PubMed=9874566;			
RA	Profit T., Moffatt S.L., Berkahn C.J., Fraser J.D.;			
RA	"Identification and characterization of novel superantigens from			
RT	Streptococcus pyogenes.";			
RL	J. Exp. Med. 189:89-102(1999).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;			
RA	MEDLINE=21192684; PubMed=11296296;			
RA	Ferretti J.J., Moshen W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
CC	-1- SUBUNIT: Binds to major histocompatibility complex class II beta			
CC	chain			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- DISEASE: Mitogenic for human peripheral blood lymphocytes.			
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN			
CC	FAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> )			
CC	-----			
DR	EMBL, AF124500; AAD30969.1; -			
DR	EMBL, AE006546; AAK33907.1; -			
DR	PDB, 1ET9; 24-MAY-00.			
DR	PDB, 1EU4; 24-MAY-00.			
DR	InterPro: IPR006123; Staph/Strep_toxin.			
DR	InterPro: IPR006126; Staph/Strep_toxin.			
DR	InterPro: IPR006173; Staph_tox_OB.			
DR	Pfam: PF02876; Staph_stp_tox_C; 1.			
DR	Pfam: PF01123; Staph_stp_toxin; 1.			
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.			
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Toxin; Signal; Complete proteome; 3D-structure.			
FT	SIGNAL	1	32	POTENTIAL.
FT	CHAIN	33	236	EXOTOXIN TYPE H.
SO	SEQUENCE	236 AA;	27485 MM;	16352923907AD40D CRC64; -
Best Match 11.5%; Score 142; DB 1; Length 236;				
Query Local Similarity 28.4%; Pred. No. 0.00038;				
Matches 69; Conservative 41; Mismatches 99; Indels 34; Gaps 15;				

Oy	2	KKI--NIKIYEII--FVILISTEET--YHOSDS--KKDISNVSDLLVATITPRDYKD	53
Dd	12	KKITSMTIICISFLLSYNVAOANSNTTNRHLESLEYLHNDSLLEAD--SIKNSP-----	63
Oy	54	CRNVEFTTHLTINIDTOKYRGCDYYIISSEMSYE-ASQEFKRDDHDVGEGLF--YLINSHTG	110
Dd	64	--DIVISHML-----KSYVDKNKLWSVFEEKDWTLSQEER-DKEVDIALSAGECEBPK	114
Oy	111	EY-IYGGITPAONKNVNHKLLGNLFISESQOOLNNKKILEEKDIYTFQEIDEFKITRYKLYMD	169
Dd	115	RYSFAFGGITTLNSEEKTEIKYVPANW--DKSKQCPMFETVAKPKPVTAQAEVDIKVKRLTIK	172
Oy	170	NKYLI-DATSPYVGRIEGIKDKKHQIDLFDSPNGSTRSDIPAKYKXNDNLIMMKNFPSH	228
Dd	173	KYDIIYNNEOKYRSKGTVLTDLNSKDIVEDLYIFGN-GDFNSMLKTYSNNERIDSTOP-H	230
Oy	229	FDI 231	
Dd	231	VDV 233	
RESULT 13			
ID	NOUG_BUCAP	STANDARD:	PRT: 910 AA.
AC	OR69Y2:		
Dt	28-FEB-2003 (Rel. 41, Created)		
Dt	28-FEB-2003 (Rel. 41, Last sequence update)		
Dt	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	NADH-quinone oxidoreductase chain G (EC 1.6.99.5) (NADH dehydrogenase I, chain G) (NDH-1, chain G).		
DN	NUOG OR BUGS152.		
OS	Buchnera aphidicola (subsp. Schiapaphis graminum).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OX	NCBI_TaxID=98794;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=22084549; PubMed=12089438;		
RX	Tamas I., Klasson L., Canback B., Naeslund A.K., Eriksson A.-S.,		
RA	Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;		
RE	"50 million years of genomic stasis in endosymbiotic bacteria.";		
	Science 296:2376-2379(2002).		
-i-	FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-sulfur (Fe-S) centers, to quinones in the respiratory chain.		
CC	Compleas the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (by similarity).		
-i-	CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.		
CC	-i- COFACTR: Binds 1 zfe-25 cluster and 1 4fe-45 cluster (potential).		
-i-	SUBUNIT: Composed of 13 different subunits. Subunits nuocD, E, F, and G constitute the peripheral sector of the complex (by similarity).		
-i-	SIMILARITY: BELONGS TO THE COMPLEX I 75 kDa SUBUNIT FAMILY.		
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CC	EMBL: AE014091; AAM67720.1; "		
DR	InterPro: IPR0000283; Complex1_75k.		
DR	InterPro: IPR001041; Ferredoxin.		
DR	Pfam: PF04879; Molybdop_Fe4S4; 1.		
DR	PFam: PF04879; Molybdop_Fe4S4; 1.		
DR	PROSITE: PS00641; COMPLEX1_75K.1; 1.		
DR	PROSITE: PS00642; COMPLEX1_75K.2; 1.		
DR	PROSITE: PS00643; COMPLEX1_75K.3; 1.		
DR	Oxidoreductase; NAD; Quinone; Metal-binding; Iron-sulfur; Iron;		
kw	2fe-25; 4fe-45; Complete proteome.		

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FT METAL 23 23 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 34 34 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 45 45 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 48 48 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 103 103 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 106 106 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 112 112 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 151 151 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 154 154 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 157 157 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 201 201 IRON-SULFUR (4FE-4S) (POTENTIAL).
SO SEQUENCE 910 AA; 104358 MW; 7F50FE2F296DA519 CRC64;

Query Match 7.8%; Score 96.5; DB 1; Length 910;
Best Local Similarity 20.5%; Pred. No. 5.5;
Matches 61; Conservative 41; Mismatches 93; Indels 103; Gaps 12;

QY 9 IVFIITVILISTYTYTHOSDKDISVKSDDLVAITTPYDKCR-----VNFS 59
DB 64 IMSCMTPIVDITISINDTSKFRSRNIVELL--TNHPDCEVCCEGNGCHLQDMTVM 120
QY 60 TTHTL-NIDPOKRGKDYISSEMSYEASQ-----KFKRD---DHVDVFG---LF 102
DB 121 TTHNFRYRPSKRTKHKNOYLGSFIKHEMNCICGRCVRYRYADGTDLDVYGANNNTY 180
QY 103 Y-----ILNSHTGEYI----- 113
DB 181 FGRIEHLGVLEHSGNLEICPTGVFTDKTHSKKYNRKMWDQYAPGICQNSICGNISIG 240
QY 114 --YGGITPAQN--NKNVHKLLGNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKYL 168
DB 241 ERVEIIRIRERHYESINHLYICDLGRFGYSTNLKRN--PKRPILSKENDVNLNF-- 296
QY 169 DNYKIYDASPVEYSGRIETGDKGHEIDLEFDSPENEGTSRSDIAKYNKRNIIIMKN 226
DB 297 -NKAIETATNFOYKKNVIGY-----GSIRSIENNFALDELVEKNEF 358

RESULT 14
ID ETEFL_YABAM STANDARD; PRT: 635 AA.
AC Q90B97;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Early transcription factor 70 kDa subunit (VETF small subunit).
GN BAR.
OS Yaba monkey tumor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OX NCBI_TaxID=38804;
RN [1]
RP SEQUENCE FROM N.A.
RA "Amano H., Morikawa S., Ueda Y., Miyamura T.;
RT "Nucleotide sequence of the central 50kbp region of Yaba virus DNA.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
CC EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
CC ASSOCIATED WITH VETF.
CC -1- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE VETF SUBFAMILY OF HELICASES.
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CC -----
CC EMBL: AB015885; BAA8798.1; -
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR002464; DEAD_box.

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DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF002471; helicase_C.1.
DR SMART: SM00487; DEXDC.1.
DR PROSITE: PS00690; DEAD_ATP_HELICASE.1.
KW Helicase; Transcription regulation; Activator; ATP-binding.
FT NP_BIND 45 52 ATP (POTENTIAL).
FT SITE 135 138 DEXH BOX.
SO SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;

Query Match 7.7%; Score 95; DB 1; Length 635;
Best Local Similarity 22.5%; Pred. No. 4.8;
Matches 56; Conservative 36; Mismatches 81; Indels 76; Gaps 13;

QY 2 KKNIVKIVFIITVILISTYTYTHOSDKDISVKSDDLVAITTPYDKCRVNFS 59
DB 272 KKNMNVSLAVIGQNFINNLDILQEDQKELYPULKSLNGILYDELT----- 319
QY 60 TTHTLNIDPOKRGKDYISSEMSYEASQKRRDHYDVGFLFYLSHSGEYIYGITP 119
DB 320 --TLNI-SSKFK--YFIGKITSLTGKQ-----FIYFSNS---TYGGLI- 354
QY 120 AQNNKVVHKLLGNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKILMPNRYKIDATSP 179
DB 355 ----IKYIMLSNGYSEYNSQGTNPKLNGKP-KTFAIYVSKMKSSLEDLVNYSOL- 407
QY 180 YVSGRIETGDKGHEIDLEFDSPENEGTS-----DIFAKYKDNRII--N 222
DB 408 -----NKDG--SQIMLFSSNIMSESYTLKEVINIMWTIPDFISQI--NQLIGRS 454
QY 223 MKNFSHFDI 231
DB 455 IRKFSYFDI 463

RESULT 15
ID TEGU_HSV6U STANDARD; PRT: 2077 AA.
AC P52340;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Large tegument protein.
GN U31 OR HHRF1.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efsthadiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution.";
RL Virology 209:29-51(1995).
CC -1- FUNCTION: TEGUMENT PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC EBV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
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CC -----
CC EMBL: X83413; CA58411.1; -
CC InterPro: IPR006928; Herpes_teg_N.
CC Pfam: PF04843; Herpes_teg_N.1.
SO SEQUENCE 2077 AA; 239946 MW; C1CA4BDC2650511 CRC64;

Query Match 7.6%; Score 94; DB 1; Length 2077;

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